

196219.ST25.txt
SEQUENCE LISTING

<110> May, Gregory
Baszczynski, Christopher
Zhu, Tong
Kipp, Peter
Mahajan, Pramod

<120> PLANT MSH2 SEQUENCES AND METHODS OF USE

<130> 5839-2 (035839/196219)

<160> 42

<170> PatentIn version 3.0

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<211> 3033

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99

Leu Pro Glu Leu Lys Leu Asp Ala Lys Gln Ala Gln Gly Phe Leu Ser
15 20 25

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147

Phe Phe Lys Thr Leu Pro Lys Asp Pro Arg Ala Val Arg Leu Phe Asp
30 35 40

cgt cgg gac tat tat aca tct cat gga gat gat gca act ttc att gca
195

Arg Arg Asp Tyr Tyr Thr Ser His Gly Asp Asp Ala Thr Phe Ile Ala
45 50 55

gag aca tat tac cac aca aca act gcg tta cga cag ttg ggt aat aga
243

Glu Thr Tyr Tyr His Thr Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg
60 65 70

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291

Ala Asp Ala Leu Ser Ser Val Ser Val Ser Arg Asn Met Phe Glu Thr
75 80 85 90

ata gct cgt gac att ctc ttg gag aga atg gac cgt act ctt gaa cta
339

Ile Ala Arg Asp Ile Leu Leu Glu Arg Met Asp Arg Thr Leu Glu Leu

95

100

105

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387

Tyr Glu Gly Ser Gly Ser Asn Trp Arg Leu Val Lys Ser Gly Thr Pro
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ggg aat ctt gga agt ttt gag gat att ctg ttt gct aat aat gaa atg
435

Gly Asn Leu Gly Ser Phe Glu Asp Ile Leu Phe Ala Asn Asn Glu Met
125 130 135

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483

Gln Asn Ser Pro Val Ile Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn
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531

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155 160 165 170

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579

Gly Leu Thr Glu Phe Leu Asp Asp Ser His Phe Thr Asn Leu Glu Ser
175 180 185

gct ttg gtt gct ctt ggt tgc aga gaa tgt ctt gta cca gcg gag act
627

Ala Leu Val Ala Leu Gly Cys Arg Glu Cys Leu Val Pro Ala Glu Thr
190 195 200

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675

Gly Lys Ser Ser Glu Tyr Arg Pro Met Phe Asp Ala Ile Ser Arg Cys
205 210 215

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723

Gly Val Met Val Thr Glu Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp
220 225 230

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771

Leu Val Gln Asp Leu Gly Arg Leu Val Lys Gly Ser Val Glu Pro Val
235 240 245 250

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819

Arg Asp Leu Val Ser Gly Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys
255 260 265

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867

Ile Leu Ser Tyr Ala Glu Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn
270 275 280

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915

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Tyr Thr Val Lys Gln Tyr Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser
 285 290 295

gct gct atg aga gca ctg aat gtt atg gag agc aaa tca gat gct aat
 963

Ala Ala Met Arg Ala Leu Asn Val Met Glu Ser Lys Ser Asp Ala Asn
 300 305 310

aaa aat ttt agc ttg ttc ggt ctg atg aat aga acg tgt act gct gga
 1011

Lys Asn Phe Ser Leu Phe Gly Leu Met Asn Arg Thr Cys Thr Ala Gly
 315 320 325 330

atg ggt aaa agg tta ttg cac atg tgg ctg aag caa cct tta cta gat
 1059

Met Gly Lys Arg Leu Leu His Met Trp Leu Lys Gln Pro Leu Leu Asp
 335 340 345

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 1107

Val Glu Glu Ile Asn Cys Arg Leu Asp Leu Val Gln Ser Phe Val Glu
 350 355 360

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 1155

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 365 370 375

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 1203

Asp Ile Glu Arg Leu Thr His Asn Leu Glu Arg Lys Arg Ala Ser Leu
 380 385 390

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 1251

Val His Val Val Lys Leu Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile
 395 400 405 410

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 1299

Lys Ser Val Leu Glu Arg His Asp Gly Gln Phe Ala Thr Leu Ile Arg
 415 420 425

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 1347

Glu Arg Tyr Ile Asp Ser Leu Glu Lys Trp Ser Asp Asp Asn His Leu
 430 435 440

aat aag ttc ata ggt ctt gtg gaa act tct gtt gac ctt gat caa ctt
 1395

Asn Lys Phe Ile Gly Leu Val Glu Thr Ser Val Asp Leu Asp Gln Leu
 445 450 455

gag aat gga gaa tac atg att tct tct gca tat gac cca aat tta tct
 1443

Glu Asn Gly Glu Tyr Met Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser
 460 465 470

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1491

Ala Leu Lys Asp Glu Gln Glu Thr Leu Glu Arg Gln Ile His Asn Leu
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1539

His Lys Gln Thr Ala Asn Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu
495 500 505

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1587

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1635

Lys Glu Glu Pro Lys Val Arg Lys Gln Leu Asn Ser His Tyr Ile Val
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1683

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540 545 550

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1731

Lys Leu Gly Asp Gln Phe Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys
555 560 565 570

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1779

Gln Lys Glu Leu Val Ala Arg Val Val Gln Thr Ala Ala Ser Phe Ser
575 580 585

gag gtg ttt gca ggt ata gct ggt gta ctt gct gag ttg gat gtg tta
1827

Glu Val Phe Ala Gly Ile Ala Gly Val Leu Ala Glu Leu Asp Val Leu
590 595 600

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1875

Leu Ser Phe Ala Asp Leu Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg
605 610 615

cca aat atc agt cca cca gat aca gga gat att ata ctt gaa ggg tgt
1923

Pro Asn Ile Ser Pro Pro Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys
620 625 630

agg cat cct tgt gtg gaa gct caa gat tgg gtt aac tcc att cct aat
1971

Arg His Pro Cys Val Glu Ala Gln Asp Trp Val Asn Ser Ile Pro Asn
635 640 645 650

gac tgt aga cta gtt agg gga gag agt tgg ttt cag att atc aca ggc
2019

Asp Cys Arg Leu Val Arg Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly
655 660 665

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cct aac atg ggt gga aag tcg acc tac att cgg cag gtt ggt gtg aat
2067

Pro Asn Met Gly Gly Lys Ser Thr Tyr Ile Arg Gln Val Gly Val Asn
670 675 680

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2115

Val Leu Met Ala Gln Val Gly Ser Phe Val Pro Cys Asp Asn Ala Thr
685 690 695

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2163

Ile Ser Ile Arg Asp Cys Ile Phe Ala Arg Val Gly Ala Gly Asp Cys
700 705 710

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2211

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750 755 760

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2355

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765 770 775

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2451

Gly His Lys Lys Asn Ala Gly Ile Ala Asn Phe His Val Phe Ala His
795 800 805 810

att gac cct tct aat cgc aag cta act atg ctt tac aag gtt cac cca
2499

Ile Asp Pro Ser Asn Arg Lys Leu Thr Met Leu Tyr Lys Val His Pro
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2595

Phe Pro Pro Ser Val Val Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu
845 850 855

gag gat ttc tct cct att gcc ata att cca aat gac att aaa gag gca
2643

Glu Asp Phe Ser Pro Ile Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala
860 865 870

gct tca aaa cgg aag aga gaa ttt gac cgc cat gac gtg tct aga ggt
2691

Ala Ser Lys Arg Lys Arg Glu Phe Asp Arg His Asp Val Ser Arg Gly
875 880 885 890

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2739

Thr Ala Arg Ala Arg Gln Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu
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2787

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2835

Thr Asp Leu Glu Arg Asp Ala Val Asp Ser His Trp Leu Gln Gln Phe
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2888
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35 40 45

Ser His Gly Asp Asp Ala Thr Phe Ile Ala Glu Thr Tyr Tyr His Thr
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Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg Ala Asp Ala Leu Ser Ser
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Val Ser Val Ser Arg Asn Met Phe Glu Thr Ile Ala Arg Asp Ile Leu
85 90 95

Leu Glu Arg Met Asp Arg Thr Leu Glu Leu Tyr Glu Gly Ser Gly Ser
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Asn Trp Arg Leu Val Lys Ser Gly Thr Pro Gly Asn Leu Gly Ser Phe
115 120 125

Glu Asp Ile Leu Phe Ala Asn Asn Glu Met Gln Asn Ser Pro Val Ile
130 135 140

Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn Gly Cys Glu Val Gly Leu
145 150 155 160

Gly Tyr Val Asp Ile Thr Lys Arg Val Leu Gly Leu Thr Glu Phe Leu
165 170 175

Asp Asp Ser His Phe Thr Asn Leu Glu Ser Ala Leu Val Ala Leu Gly
180 185 190

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195 200 205

Arg Pro Met Phe Asp Ala Ile Ser Arg Cys Gly Val Met Val Thr Glu
210 215 220

Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp Leu Val Gln Asp Leu Gly
225 230 235 240

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245 250 255

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260 265 270

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305 310 315 320

Gly Leu Met Asn Arg Thr Cys Thr Ala Gly Met Gly Lys Arg Leu Leu
325 330 335

His Met Trp Leu Lys Gln Pro Leu Leu Asp Val Glu Glu Ile Asn Cys
340 345 350

Arg Leu Asp Leu Val Gln Ser Phe Val Glu Asp Ala Ala Leu Arg Gln
355 360 365

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370 375 380

His Asn Leu Glu Arg Lys Arg Ala Ser Leu Val His Val Val Lys Leu
385 390 395 400

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405 410 415

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Leu Glu Lys Trp Ser Asp Asp Asn His Leu Asn Lys Phe Ile Gly Leu
435 440 445

Val Glu Thr Ser Val Asp Leu Asp Gln Leu Glu Asn Gly Glu Tyr Met
450 455 460

Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser Ala Leu Lys Asp Glu Gln
465 470 475 480

Glu Thr Leu Glu Arg Gln Ile His Asn Leu His Lys Gln Thr Ala Asn
485 490 495

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500 505 510

Gln Phe Gly His Val Phe Arg Ile Thr Lys Lys Glu Glu Pro Lys Val

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520

525

Arg Lys Gln Leu Asn Ser His Tyr Ile Val Leu Glu Thr Arg Lys Asp
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Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys Lys Leu Gly Asp Gln Phe
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580 585 590

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610 615 620

Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys Arg His Pro Cys Val Glu
625 630 635 640

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645 650 655

Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly Pro Asn Met Gly Gly Lys
660 665 670

Ser Thr Tyr Ile Arg Gln Val Gly Val Asn Val Leu Met Ala Gln Val
675 680 685

Gly Ser Phe Val Pro Cys Asp Asn Ala Thr Ile Ser Ile Arg Asp Cys
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705 710 715 720

Thr Phe Met Gln Glu Met Leu Glu Thr Ala Ser Ile Leu Lys Gly Ala
725 730 735

Thr Asp Arg Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg Gly Thr Ser
740 745 750

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Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala Thr His Phe His Glu Leu
 770 775 780

Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn Gly His Lys Lys Asn Ala
 785 790 795 800

Gly Ile Ala Asn Phe His Val Phe Ala His Ile Asp Pro Ser Asn Arg
 805 810 815

Lys Leu Thr Met Leu Tyr Lys Val His Pro Gly Ala Cys Asp Gln Ser
 820 825 830

Phe Gly Ile His Val Ala Glu Phe Ala Asn Phe Pro Pro Ser Val Val
 835 840 845

Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu Glu Asp Phe Ser Pro Ile
 850 855 860

Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala Ala Ser Lys Arg Lys Arg
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Glu Phe Asp Arg His Asp Val Ser Arg Gly Thr Ala Arg Ala Arg Gln
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Leu	Pro	Glu	Leu	Lys 15	Leu	Asp	Ala	Lys	Gln 20	Ala	Gln	Gly	Phe	Leu 25	Ser
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Phe	Phe	Lys	Thr 30	Leu	Pro	Lys	Asp	Pro 35	Arg	Ala	Val	Arg	Leu 40	Phe	Asp
cgt 195	cgg	gac	tat	tat	act	gct	cat	gga	gat	gat	gca	act	ttc	att	gca
Arg	Arg	Asp 45	Tyr	Tyr	Thr	Ala	His 50	Gly	Asp	Asp	Ala	Thr 55	Phe	Ile	Ala
gag 243	aca	tat	tac	cac	aca	aca	act	gcg	tta	cga	cag	ttg	ggg	aat	aga
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Ala 75	Asp	Ala	Leu	Ser	Ser 80	Val	Ser	Val	Ser	Arg 85	Asn	Met	Phe	Glu	Thr 90
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Ile	Ala	Arg	Asp	Ile 95	Leu	Leu	Glu	Arg	Met 100	Asp	Arg	Thr	Leu	Glu 105	Leu
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Gly	Asn	Leu 125	Gly	Ser	Phe	Glu	Asp 130	Ile	Leu	Phe	Ala	Asn 135	Asn	Glu	Met
caa 483	aat	tct	ccg	gtg	att	gct	gct	ctt	gct	cca	aac	ttc	ggg	cag	aat
Gln	Asn 140	Ser	Pro	Val	Ile	Ala 145	Ala	Leu	Ala	Pro	Asn 150	Phe	Gly	Gln	Asn
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Gly 155	Cys	Glu	Val	Gly	Leu 160	Gly	Tyr	Val	Asp	Ile 165	Thr	Lys	Arg	Val	Leu 170
ggt 579	tta	aca	gaa	ttt	cta	gat	gat	agc	cac	ttc	aca	aat	ttg	gag	tct
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627

Ala Leu Val Ala Leu Gly Cys Arg Glu Cys Leu Val Pro Ala Glu Thr
190 195 200

ggc aaa tcc agt gaa tac agg cct atg ttt gat gca ata tct aga tgc
675

Gly Lys Ser Ser Glu Tyr Arg Pro Met Phe Asp Ala Ile Ser Arg Cys
205 210 215

ggc gtg atg gta act gaa aga aag aaa act gaa ttt aaa ggg aga gat
723

Gly Val Met Val Thr Glu Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp
220 225 230

ttg gta cag gat ctt ggt agg ctc gtc aag ggt tca gta gaa cct gtt
771

Leu Val Gln Asp Leu Gly Arg Leu Val Lys Gly Ser Val Glu Pro Val
235 240 245 250

cga gat ttg gtc tct ggg ttc gaa tgt gca tca ggc gct ttg ggg tgc
819

Arg Asp Leu Val Ser Gly Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys
255 260 265

ata ctt tct tat gca gaa cta ctt gcg gat gag agc aac tat gga aac
867

Ile Leu Ser Tyr Ala Glu Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn
270 275 280

tat aca gtc aaa caa tac aac ctc aat agt tac atg aga tta gat tct
915

Tyr Thr Val Lys Gln Tyr Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser
285 290 295

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963

Ala Ala Met Arg Ala Leu Asn Val Met Glu Ser Lys Ser Asp Ala Asn
300 305 310

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1011

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1059

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335 340 345

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1107

Val Glu Glu Ile Asn Cys Arg Leu Asp Leu Val Gln Ser Phe Val Glu
350 355 360

gat gct gcg ctt cgc caa gat ttg agg cag cat ctg aaa aga att tca
1155

Asp Ala Ala Leu Arg Gln Asp Leu Arg Gln His Leu Lys Arg Ile Ser
365 370 375

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1203

Asp Ile Glu Arg Leu Thr His Asn Leu Glu Arg Lys Arg Ala Ser Leu
380 385 390

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1251

Val His Val Val Lys Leu Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile
395 400 405 410

aaa agt gtt ttg gaa cgt cat gat ggg caa ttt gca aca ctc atc agg
1299

Lys Ser Val Leu Glu Arg His Asp Gly Gln Phe Ala Thr Leu Ile Arg
415 420 425

gaa agg tat att gat tct cta gag aaa tgg agt gat gat aat cac ctg
1347

Glu Arg Tyr Ile Asp Ser Leu Glu Lys Trp Ser Asp Asp Asn His Leu
430 435 440

aat aag ttc ata ggt ctt gtg gaa act tct gtt gac ctt gat caa ctt
1395

Asn Lys Phe Ile Gly Leu Val Glu Thr Ser Val Asp Leu Asp Gln Leu
445 450 455

gag aat gga gaa tac atg att tct tct gca tat gac cca aat tta tct
1443

Glu Asn Gly Glu Tyr Met Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser
460 465 470

gct ctg aag gat gag caa gag aca ttg gag cga caa att cat aat ttg
1491

Ala Leu Lys Asp Glu Gln Glu Thr Leu Glu Arg Gln Ile His Asn Leu
475 480 485 490

cac aaa caa act gcc aat gat ctt gat cta cct att gat aag tca ctt
1539

His Lys Gln Thr Ala Asn Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu
495 500 505

aaa cta gat aaa gaa aca caa ttt gga cac gtc ttc aga att acc aag
1587

Lys Leu Asp Lys Glu Thr Gln Phe Gly His Val Phe Arg Ile Thr Lys
510 515 520

aaa gaa gaa cca aaa gtc agg aag cag cta aat tct cac tac att gtt
1635

Lys Glu Glu Pro Lys Val Arg Lys Gln Leu Asn Ser His Tyr Ile Val
525 530 535

ctc gaa aca cgt aag gat ggg gta aag ttc acc tat aca aaa ctc aaa
1683

Leu Glu Thr Arg Lys Asp Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys
540 545 550

aaa cta gga gat cag ttc cag aag att gta gag gag tac aaa agc tgt
1731

Lys Leu Gly Asp Gln Phe Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys

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555                               560                               565                               570
cag aaa gaa ttg gta gct cgt gta gtt caa aca gct gcg agt ttc tcc
1779
Gln Lys Glu Leu Val Ala Arg Val Val Gln Thr Ala Ala Ser Phe Ser
575                               580                               585

gag gtg ttt gca ggt ata gct ggt gta ctt gct gag ttg gat gtg tta
1827
Glu Val Phe Ala Gly Ile Ala Gly Val Leu Ala Glu Leu Asp Val Leu
590                               595                               600

ctg agt ttt gcg gat ttg gct gcc agt tgc cca act ccc tac aca aga
1875
Leu Ser Phe Ala Asp Leu Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg
605                               610                               615

cca aat atc agt cca cca gat aca gga gat att ata ctt gaa ggg tgt
1923
Pro Asn Ile Ser Pro Pro Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys
620                               625                               630

agg cat cct tgt gtg gaa gct caa gat tgg gtt aac tcc att cct aat
1971
Arg His Pro Cys Val Glu Ala Gln Asp Trp Val Asn Ser Ile Pro Asn
635                               640                               645                               650

gac tgt aga cta gtt agg gga gag agt tgg ttt cag att atc aca ggc
2019
Asp Cys Arg Leu Val Arg Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly
655                               660                               665

cct aac atg ggt gga aag tcg acc tac att cgg cag gtt ggt gtg aat
2067
Pro Asn Met Gly Gly Lys Ser Thr Tyr Ile Arg Gln Val Gly Val Asn
670                               675                               680

gtc ctg atg gcc caa gtt ggc tcg ttt gtt cca tgt gac aat gct acc
2115
Val Leu Met Ala Gln Val Gly Ser Phe Val Pro Cys Asp Asn Ala Thr
685                               690                               695

att tct att cgt gat tgt att ttt gct cgt gtt ggc gct gga gat tgc
2163
Ile Ser Ile Arg Asp Cys Ile Phe Ala Arg Val Gly Ala Gly Asp Cys
700                               705                               710

cag ctg aga gga gtt tct act ttt atg caa gag atg ctt gag act gca
2211
Gln Leu Arg Gly Val Ser Thr Phe Met Gln Glu Met Leu Glu Thr Ala
715                               720                               725                               730

tcg atc ttg aaa gga gct act gat aga tca ttg att ata att gat gag
2259
Ser Ile Leu Lys Gly Ala Thr Asp Arg Ser Leu Ile Ile Ile Asp Glu
735                               740                               745

ttg ggc cgt ggg aca tca acc tac gat ggc ttt ggt tta gct tgg gct
2307

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Leu Gly Arg Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala
 750 755 760

att tgt gag cac att gtt gaa gaa att aaa gca cca aca ttg ttt gcc
 2355

Ile Cys Glu His Ile Val Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala
 765 770 775

act cac ttt cat gag ctg act gca tta gcc aac aag aat gga gac aat
 2403

Thr His Phe His Glu Leu Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn
 780 785 790

gga cat aag aaa aat gct ggg ata gca aat ttt cat gtt ttt gca cac
 2451

Gly His Lys Lys Asn Ala Gly Ile Ala Asn Phe His Val Phe Ala His
 795 800 805 810

att gac cct tct aat cgc aag cta act atg ctt tac aag gtt cac cca
 2499

Ile Asp Pro Ser Asn Arg Lys Leu Thr Met Leu Tyr Lys Val His Pro
 815 820 825

ggg gct tgt gat cag agt ttt ggt att cat gtt gct gaa ttt gca aat
 2547

Gly Ala Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu Phe Ala Asn
 830 835 840

ttt cca ccg agt gtt gtg gct ctg gct aga gaa aag gca tct gag ttg
 2595

Phe Pro Pro Ser Val Val Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu
 845 850 855

gag gat ttc tot cct att gcc ata att cca aat gac att aaa gag gca
 2643

Glu Asp Phe Ser Pro Ile Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala
 860 865 870

gct tca aaa cgg aag aga gaa ttt gac cgc cat gac gtg tct aga ggt
 2691

Ala Ser Lys Arg Lys Arg Glu Phe Asp Arg His Asp Val Ser Arg Gly
 875 880 885 890

act gcc aga gct cgg caa ttc tta cag gat ttc gct cag ttg cca ctg
 2739

Thr Ala Arg Ala Arg Gln Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu
 895 900 905

gat aag atg gat cca aac gtg gtc agg caa aag ttg agc aaa atg aaa
 2787

Asp Lys Met Asp Pro Asn Val Val Arg Gln Lys Leu Ser Lys Met Lys
 910 915 920

acc gac ctg gag agg gat gca gtt gac tct cac tgg ctt cag caa ttc
 2835

Thr Asp Leu Glu Arg Asp Ala Val Asp Ser His Trp Leu Gln Gln Phe
 925 930 935

ttt taattcttca gattagaact atcttctatt ctgtgaagct tgggggggaa

2888
Phe

tgatacttat gggttttgtg gatataactt agcctatctg taaactttca tttaaactcct
2948

taccccaaac atgattctct gtaatcaggg gacttttgta tgcattctgt gttaatagta
3008

agcgttatct tatatgggtca aaaaa
3033

<210> 4
<211> 939
<212> PRT
<213> Nicotiana tabacum

<400> 4

Met Asn Glu Asn Leu Glu Glu Gln Ser Lys Leu Pro Glu Leu Lys Leu
1 5 10 15

Asp Ala Lys Gln Ala Gln Gly Phe Leu Ser Phe Phe Lys Thr Leu Pro
20 25 30

Lys Asp Pro Arg Ala Val Arg Leu Phe Asp Arg Arg Asp Tyr Tyr Thr
35 40 45

Ala His Gly Asp Asp Ala Thr Phe Ile Ala Glu Thr Tyr Tyr His Thr
50 55 60

Thr Thr Ala Leu Arg Gln Leu Gly Asn Arg Ala Asp Ala Leu Ser Ser
65 70 75 80

Val Ser Val Ser Arg Asn Met Phe Glu Thr Ile Ala Arg Asp Ile Leu
85 90 95

Leu Glu Arg Met Asp Arg Thr Leu Glu Leu Tyr Glu Gly Ser Gly Ser
100 105 110

Asn Trp Arg Leu Val Lys Ser Gly Thr Pro Gly Asn Leu Gly Ser Phe
115 120 125

Glu Asp Ile Leu Phe Ala Asn Asn Glu Met Gln Asn Ser Pro Val Ile
130 135 140

Ala Ala Leu Ala Pro Asn Phe Gly Gln Asn Gly Cys Glu Val Gly Leu
145 150 155 160

Gly Tyr Val Asp Ile Thr Lys Arg Val Leu Gly Leu Thr Glu Phe Leu
 165 170 175

Asp Asp Ser His Phe Thr Asn Leu Glu Ser Ala Leu Val Ala Leu Gly
 180 185 190

Cys Arg Glu Cys Leu Val Pro Ala Glu Thr Gly Lys Ser Ser Glu Tyr
 195 200 205

Arg Pro Met Phe Asp Ala Ile Ser Arg Cys Gly Val Met Val Thr Glu
 210 215 220

Arg Lys Lys Thr Glu Phe Lys Gly Arg Asp Leu Val Gln Asp Leu Gly
 225 230 235 240

Arg Leu Val Lys Gly Ser Val Glu Pro Val Arg Asp Leu Val Ser Gly
 245 250 255

Phe Glu Cys Ala Ser Gly Ala Leu Gly Cys Ile Leu Ser Tyr Ala Glu
 260 265 270

Leu Leu Ala Asp Glu Ser Asn Tyr Gly Asn Tyr Thr Val Lys Gln Tyr
 275 280 285

Asn Leu Asn Ser Tyr Met Arg Leu Asp Ser Ala Ala Met Arg Ala Leu
 290 295 300

Asn Val Met Glu Ser Lys Ser Asp Ala Asn Lys Asn Phe Ser Leu Phe
 305 310 315 320

Gly Leu Met Asn Arg Thr Cys Thr Ala Gly Met Gly Lys Arg Leu Leu
 325 330 335

His Met Trp Leu Lys Gln Pro Leu Leu Asp Val Glu Glu Ile Asn Cys
 340 345 350

Arg Leu Asp Leu Val Gln Ser Phe Val Glu Asp Ala Ala Leu Arg Gln
 355 360 365

Asp Leu Arg Gln His Leu Lys Arg Ile Ser Asp Ile Glu Arg Leu Thr
 370 375 380

His Asn Leu Glu Arg Lys Arg Ala Ser Leu Val His Val Val Lys Leu

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385                      390                      395                      400

Tyr Gln Ser Ser Thr Arg Val Pro Tyr Ile Lys Ser Val Leu Glu Arg
      405                      410                      415

His Asp Gly Gln Phe Ala Thr Leu Ile Arg Glu Arg Tyr Ile Asp Ser
      420                      425                      430

Leu Glu Lys Trp Ser Asp Asp Asn His Leu Asn Lys Phe Ile Gly Leu
      435                      440                      445

Val Glu Thr Ser Val Asp Leu Asp Gln Leu Glu Asn Gly Glu Tyr Met
      450                      455                      460

Ile Ser Ser Ala Tyr Asp Pro Asn Leu Ser Ala Leu Lys Asp Glu Gln
      465                      470                      475

Glu Thr Leu Glu Arg Gln Ile His Asn Leu His Lys Gln Thr Ala Asn
      485                      490                      495

Asp Leu Asp Leu Pro Ile Asp Lys Ser Leu Lys Leu Asp Lys Glu Thr
      500                      505                      510

Gln Phe Gly His Val Phe Arg Ile Thr Lys Lys Glu Glu Pro Lys Val
      515                      520                      525

Arg Lys Gln Leu Asn Ser His Tyr Ile Val Leu Glu Thr Arg Lys Asp
      530                      535                      540

Gly Val Lys Phe Thr Tyr Thr Lys Leu Lys Lys Leu Gly Asp Gln Phe
      545                      550                      555                      560

Gln Lys Ile Val Glu Glu Tyr Lys Ser Cys Gln Lys Glu Leu Val Ala
      565                      570                      575

Arg Val Val Gln Thr Ala Ala Ser Phe Ser Glu Val Phe Ala Gly Ile
      580                      585                      590

Ala Gly Val Leu Ala Glu Leu Asp Val Leu Leu Ser Phe Ala Asp Leu
      595                      600                      605

Ala Ala Ser Cys Pro Thr Pro Tyr Thr Arg Pro Asn Ile Ser Pro Pro
      610                      615                      620

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Asp Thr Gly Asp Ile Ile Leu Glu Gly Cys Arg His Pro Cys Val Glu
625 630 635 640

Ala Gln Asp Trp Val Asn Ser Ile Pro Asn Asp Cys Arg Leu Val Arg
645 650 655

Gly Glu Ser Trp Phe Gln Ile Ile Thr Gly Pro Asn Met Gly Gly Lys
660 665 670

Ser Thr Tyr Ile Arg Gln Val Gly Val Asn Val Leu Met Ala Gln Val
675 680 685

Gly Ser Phe Val Pro Cys Asp Asn Ala Thr Ile Ser Ile Arg Asp Cys
690 695 700

Ile Phe Ala Arg Val Gly Ala Gly Asp Cys Gln Leu Arg Gly Val Ser
705 710 715 720

Thr Phe Met Gln Glu Met Leu Glu Thr Ala Ser Ile Leu Lys Gly Ala
725 730 735

Thr Asp Arg Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg Gly Thr Ser
740 745 750

Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Cys Glu His Ile Val
755 760 765

Glu Glu Ile Lys Ala Pro Thr Leu Phe Ala Thr His Phe His Glu Leu
770 775 780

Thr Ala Leu Ala Asn Lys Asn Gly Asp Asn Gly His Lys Lys Asn Ala
785 790 795 800

Gly Ile Ala Asn Phe His Val Phe Ala His Ile Asp Pro Ser Asn Arg
805 810 815

Lys Leu Thr Met Leu Tyr Lys Val His Pro Gly Ala Cys Asp Gln Ser
820 825 830

Phe Gly Ile His Val Ala Glu Phe Ala Asn Phe Pro Pro Ser Val Val
835 840 845

Ala Leu Ala Arg Glu Lys Ala Ser Glu Leu Glu Asp Phe Ser Pro Ile
850 855 860

Ala Ile Ile Pro Asn Asp Ile Lys Glu Ala Ala Ser Lys Arg Lys Arg
865 870 875 880

Glu Phe Asp Arg His Asp Val Ser Arg Gly Thr Ala Arg Ala Arg Gln
885 890 895

Phe Leu Gln Asp Phe Ala Gln Leu Pro Leu Asp Lys Met Asp Pro Asn
900 905 910

Val Val Arg Gln Lys Leu Ser Lys Met Lys Thr Asp Leu Glu Arg Asp
915 920 925

Ala Val Asp Ser His Trp Leu Gln Gln Phe Phe
930 935

<210> 5
<211> 160
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 5
nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaaccacaca tccctccatt
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ttcccattac tctataaaat cctttgcttt tcatttctac tgcagaaaag ttaaaagaaa
120

aaaaaaaaatg aatgaaaatt tggaggaaca gagcaagctt
160

<210> 6
<211> 163
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (1)..(2)
<223> "n" at positions 1 and 2 can be A, C, G, or T

<220>
<221> unsure
<222> (141)..(141)
<223> "n" at position 141 can be A, C, G, or T

<400> 6
 nnaagagaat cttctctagc tccccgccat tctctttccc gccaaaccac atccctccat
 60

tttccatta ctctataaaa tcctttgctt ttcattttcta ctgcagaaaa gtttaaagaa
 120

aaaaaaaaat gaatgaaaat ntggaggaac agagcaagct tca
 163

<210> 7
 <211> 163
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> unsure
 <222> (1)..(2)
 <223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 7
 nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaaccacaca tccctccgtt
 60

ttcccattac tctataaaat cctttgcttt tcattttctac tgcagaaaag ttaaaagaaa
 120

aaaaaaaaaaa tgaatgaaaa tttggaggaa cagagcaagc ttc
 163

<210> 8
 <211> 165
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> unsure
 <222> (1)..(2)
 <223> "n" at positions 1 and 2 can be A, C, G, or T

<220>
 <221> unsure
 <222> (161)..(161)
 <223> "n" at position 161 can be A, C, G, or T

<400> 8
 nnttctctag ctccccgccca ttctctttcc cgccaatcca aatccctcca ttttctctta
 60

ttttccatt actctataaaa atcctttcct tttcattttct acagcataaaa ggtaaagaa
 120

aaaaaaatga atgaaaattt ggaggaacag agcaagttca ncgaa

165

<210> 9
 <211> 166
 <212> DNA
 <213> Nicotiana tabacum

 <220>
 <221> unsure
 <222> (165)..(166)
 <223> "n" at positions 165 abd 166 can be A, C, G, or T

<400> 9
 agagaatctt ctctagctcc ccgccattct cttcccgcc aatccaagtc cctccatttt
 60

cctctatttt cccattactc tataaaatcc tttccttttc atttctacag cataaagggt
 120

aaagaaaaaa aaatgaatga aaatttggag gaacagagca agctnn
 166

<210> 10
 <211> 166
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> unsure
 <222> (1)..(2)
 <223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 10
 nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaaccaca tccctccatt
 60

ttcccattac tctataaaat cctttgcttt tcatttctac tgcagaaaag ttaaagaaa
 120

aaaaaaatg aatgaaaatt tggaggaaca gagcaagctt caatcg
 166

<210> 11
 <211> 166
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> unsure
 <222> (1)..(2)
 <223> "n" at positions 1 and 2 can be A, C, G, or T

<220>

<221> unsure
 <222> (157)..(158)
 <223> "n" at positions 157 and 158 can be A, C, G, or T

<400> 11
 nnagagaatc ttctctagct ccccgccatt ctctttcccg ccaaccacaca tccctccatt
 60

ttcccattac tctataaaat cctttgcttt tcattttctac tgcagaaaag ttaaaagaaa
 120

aaaaaaaatg aatgaaaatt tggaggaaca gagcaanntt caatcg
 166

<210> 12
 <211> 165
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> unsure
 <222> (1)..(2)
 <223> "n" at positions 1 and 2 can be A, C, G, or T

<400> 12
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 60

ttcccattac tctataaaat cctttgcttt tcattttctac tgcagaaaag ttaaaagaaa
 120

aaaaaatgaa tgaaaatttg gaggaacaga gcaagcttca atcga
 165

<210> 13
 <211> 314
 <212> DNA
 <213> Nicotiana tabacum

<220>
 <221> unsure
 <222> (222)..(222)
 <223> "n" at position 222 can be A, C, G, or T

<400> 13
 gatataccta gtgattcttt gcaatgaaag ttgcatcatc tccatgagca gtataatagt
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cccgacgatc aaagaggcga actgccctag ggtccttggg tagggttttg aaaaatgaga
 120

gaaatccttg agcttgctta gcatcaagtt taagctcagg aagcttgctc tgttcctcca
 180

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aaatcgaatt cccgcggccg ccatggcggc cgggagcatg cnacgtcggg cccaattcgc
240

cctatagtga gtcgtattac aattcactgg cgcgtgtttt acaacgtcgt gactgggaaa
300

accctggcgt tacc
314

<210> 14
<211> 314
<212> DNA
<213> Nicotiana tabacum

<400> 14
gatataccta gtgattcttt gcaatgaaag ttgcatcatc tccatgagca gtataatagt
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cccgcagatc aaagaggcga actgccctag ggtccttggg cagggttttg aagaatgaga
120

gaaatccttg agcttgctta gcatccagtt taagctcggg aagcttgctc tgttcctcca
180

aaatcgaatt cccgcggccg ccatggcggc cgggagcatg ccgacgtcgg gcccaattcg
240

ccctatagtg agtcgtatta caattcactg gccgtcgttt tacaacgtcg tgactgggaa
300

aaccctggcg ttac
314

<210> 15
<211> 311
<212> DNA
<213> Nicotiana tabacum

<400> 15
atatcactag tgattctttg caatgaaagt tgcatactct ccatgagatg tataatagtc
60

ccgacgatca aagaggcgaa ctgccctagg gtccttgggc aggtttttga agaagagag
120

aaatccttga gcttgcttag catccagttt aagctcggga agcttgctct gttcctccaa
180

aatcgaattc ccgcggccgc catggcggcc gggagcatgc gacgtcgggc ccaattcgcc
240

ctatagttag tcgtattaca attcactggc cgtcgtttta caacgtcgtg actgggaaaa
300

ccctggcggtt a
311

<210> 16
 <211> 214
 <212> DNA
 <213> Nicotiana tabacum

<400> 16
 gttaaaccct aattcgtaa atgttttatt acattttcag aagtttattc ttacaagtct
 60

tttctagctc taatttttta ttatttactt tttctcttca tattatttat tgtgtttaat
 120

aaatagaggg ttcattattag ttgttcagct gatttaggga ttttaaccgta gtttgattga
 180

ttgaaatttg ttaccgtgaa tggttttgtt ttag
 214

<210> 17
 <211> 223
 <212> DNA
 <213> Nicotiana tabacum

<400> 17
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 60

ttttctagtt ctaatttttt ttattttata gtttttctct ttatattggt tactgtgttt
 120

aataaatgga tattgatggt tcatattagc ggttcaactg atttggggat ttaactgtag
 180

tttgattgat tgatatttgt tattgtgaat ggtcttggtt tag
 223

<210> 18
 <211> 222
 <212> DNA
 <213> Nicotiana tabacum

<400> 18
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 60

ttttctagtt ctaatttttt ttattttata gtttttctct ttatattggt tactgtgttt
 120

aataaatgga tattgatggt tcatattagc ggttcaactg atttggggat ttaactgtag
 180

tttgattgat gatatttgt attgtgaatg gttttgtttt ag
 222

<210> 19

<211> 107
<212> DNA
<213> Nicotiana tabacum

<400> 19
gtaacttttt catattattc attctgttta aatagttatt gcaccttcac ttgtagagaa
60

aattgctcgg cggttcactt aatagagaac ttttgatttt ttgacg
107

<210> 20
<211> 105
<212> DNA
<213> Nicotiana tabacum

<400> 20
gtaacttttt catattattc attctgttta aatagttatt gcaccttcac ttgtagagaa
60

aattgtagt cgggttgctt aatagagaac tctttttttt tgcag
105

<210> 21
<211> 106
<212> DNA
<213> Nicotiana tabacum

<220>
<221> unsure
<222> (11)..(16)
<223> "n" at positions 11-16 can be A, C, G, or T

<400> 21
gtaacttttt nnnnnnattc attctgttca aacggttatt gcaccttcac ttgtagagaa
60

aattgtagt cgggttgctt aatagagaac tctttttttt ttgacg
106

<210> 22
<211> 5
<212> PRT
<213> MutS consensus sequence

<400> 22

Thr Gly Pro Asn Met
1 5

<210> 23
<211> 5
<212> PRT
<213> MutS consensus sequence

<400> 23

Phe Ala Thr His Tyr
1 5

<210> 24

<211> 20

<212> DNA

<213> oligonucleotide primer

<400> 24

gtaacagggc ctaacatggg
20

<210> 25

<211> 19

<212> DNA

<213> oligonucleotide primer

<400> 25

ggaagtgagt agcaaacag
19

<210> 26

<211> 19

<212> DNA

<213> oligonucleotide primer

<400> 26

caggccctaa catgggtgg
19

<210> 27

<211> 20

<212> DNA

<213> oligonucleotide primer

<400> 27

aatgaaatgc aagattctcc
20

<210> 28

<211> 20

<212> DNA

<213> oligonucleotide primer

<400> 28

gaagcttgct ctgttcctcc
20

<210> 29

<211> 17

<212> DNA

<213> oligonucleotide primer

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> "n" at position 3 can be A, C, G, or T

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> "n" at position 6 can be A, C, G, or T

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> "n" at position 9 can be A, C, G, or T

<400> 29
 acnggncna ayatggg
 17

<210> 30
 <211> 17
 <212> DNA
 <213> oligonucleotide primer

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> "n" at position 9 can be A, C, G, or T

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> "n" at position 12 can be A, C, G, or T

<400> 30
 tgyaartgng tncgraa
 17

<210> 31
 <211> 19
 <212> DNA
 <213> oligonucleotide primer

<400> 31
 caggccctaa catgggtgg
 19

<210> 32
 <211> 6
 <212> PRT

<213> MSH2 consensus sequence

<400> 32

Asp Tyr Tyr Thr Ala His
1 5

<210> 33

<211> 20

<212> DNA

<213> oligonucleotide primer

<400> 33

gattattata cagctcatgg
20

<210> 34

<211> 6

<212> PRT

<213> MSH2 consensus sequence

<400> 34

Met Trp Leu Lys Gln Pro
1 5

<210> 35

<211> 17

<212> DNA

<213> oligonucleotide primer

<400> 35

atgtggctga aacaacc
17

<210> 36

<211> 22

<212> DNA

<213> oligonucleotide primer

<400> 36

cttatgtcca ttgtctccat tc
22

<210> 37

<211> 20

<212> DNA

<213> oligonucleotide primer

<400> 37

gtccattgtc tccattcttg
20

<210> 38

<211> 20

<212> DNA
<213> oligonucleotide primer

<400> 38
gcaccccaaa gcgcctgatg
20

<210> 39
<211> 23
<212> DNA
<213> oligonucleotide primer

<400> 39
ctgatgcaca ttcgaaccga gag
23

<210> 40
<211> 22
<212> DNA
<213> oligonucleotide primer

<400> 40
acatatagtt caagagtacg gt
22

<210> 41
<211> 22
<212> DNA
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<400> 41
gctattgttt caaacatggt tc
22

<210> 42
<211> 22
<212> DNA
<213> oligonucleotide primer

<400> 42
ttggaggaac agagcaagct tc
22